```
  1 ATTTTATTTATTACCAATCTTATATAATATATTAAATTTCTCTTACAAAAATCTCTAATG   60
 61 TTTTATACCTAATATATATATTCTGGCTTGTATCTACTTTGCACTTCCACTATTGTTAAT  120
121 TTATTTTCACTATTTTAGGTGTAATATGAATTGCAAAAAAATTCTTATAACAACTGCATT  180
                             M  N  C  K  K  I  L  I  T  T  A  L

181 AATATCATTAATGTACTCTATTCCAAGCATATCTTTTTCTGATACTATACAAGATGGTAA  240
     I  S  L  M  Y  S  I  P  S  I  S  F  S  D  T  I  Q  D  G  N

241 CATGGGTGGTAACTTCTATATTAGTGGAAAGTATGTACCAAGTGTCTCACATTTTGGTAG  300
     M  G  G  N  F  Y  I  S  G  K  Y  V  P  S  V  S  H  F  G  S

301 CTTCTCAGCTAAAGAAGAAAGCAAATCAACTGTTGGAGTTTTTGGATTAAAACATGATTG  360
     F  S  A  K  E  E  S  K  S  T  V  G  V  F  G  L  K  H  D  W

361 GGATGGAAGTCCAATACTTAAGAATAAACACGCTGACTTTACTGTTCCAAACTATTCGTT  420
     D  G  S  P  I  L  K  N  K  H  A  D  F  T  V  P  N  Y  S  F

421 CAGATACGAGAACAATCCATTTCTAGGGTTTGCAGGAGCTATCGGTTACTCAATGGGTGG  480
     R  Y  E  N  N  P  F  L  G  F  A  G  A  I  G  Y  S  M  G  G

481 CCCAAGAATAGAATTCGAAATATCTTATGAAGCATTCGACGTAAAAAGTCCTAATATCAA  540
     P  R  I  E  F  E  I  S  Y  E  A  F  D  V  K  S  P  N  I  N

541 TTATCAAAATGACGCGCACAGGTACTGCGCTCTATCTCATCACACATCGGCAGCCATGGA  600
     Y  Q  N  D  A  H  R  Y  C  A  L  S  H  H  T  S  A  A  M  E

601 AGCTGATAAATTTGTCTTCTTAAAAAACGAAGGGTTAATTGACATATCACTTGCAATAAA  660
     A  D  K  F  V  F  L  K  N  E  G  L  I  D  I  S  L  A  I  N

661 TGCATGTTATGATATAATAAATGACAAAGTACCTGTTTCTCCTTATATATGCGCAGGTAT  720
     A  C  Y  D  I  I  N  D  K  V  P  V  S  P  Y  I  C  A  G  I
```

Fig. 1A

```
 721 TGGTACTGATTTGATTTCTATGTTTGAAGCTACAAGTCCTAAAATTTCCTACCAAGGAAA  780
      G  T  D  L  I  S  M  F  E  A  T  S  P  K  I  S  Y  Q  G  K

 841 CAGGATCATAGGTAATGAGTTTAGAGATATTCCTGCAATAGTACCTAGTAACTCAACTAC  900
      R  I  I  G  N  E  F  R  D  I  P  A  I  V  P  S  N  S  T  T

 901 AATAAGTGGACCACAATTTGCAACAGTAACACTAAATGTGTGTCACTTTGGTTTAGAACT  960
      I  S  G  P  Q  F  A  T  V  T  L  N  V  C  H  F  G  L  E  L

 961 TGGAGGAAGATTTAACTTCTAATTTTATTGTTGCCACATATTAAAAATGATCTAAACTTG 1020
      G  G  R  F  N  F (SEQ. ID NO: 2)
1021 TTTTTAWTATTGCTACATACAAAAAAAGAAAAATAGTGGCAAAAGAATGTAGCAATAAGA 1080
1081 GGGGGGGGGGGACCAAATTTATCTTCTATGCTTCCCAAGTTTTTTCYCGCTATTTATGA 1140
1141 CTTAAACAACAGAAGGTAATATCCTCACGGAAAACTTATCTTCAAATATTTTATTTATTA 1200
1201 CCAATCTTATATAATATATTAAATTTCTCTTACAAAAATCACTAGTATTTTATACCAAAA 1260
1261 TATATATTCTGACTTGCTTTTCTTCTGCACTTCTACTATTTTTAATTTATTTGTCACTAT 1320
1321 TAGGTTATAATAAWATGAATTGCMAAAGATTTTTCATAGCAAGTGCATTGATATCACTAA 1380
1381 TGTCTTTCTTACCTAGCGTATCTTTTTCTGAATCAATACATGAAGATAATATAAATGGTA 1440
1441 ACTTTTACATTAGTGCAAAGTATATGCCAAGTGCCTCACACTTTGGCGTATTTTCAGTTA 1500
1501 AAGAAGAGAAAAACACAACAACTGGAGTTTTCGGATTAAAACAAGATTGGGACGGAGCAA 1560
1561 CACTAAAGGATGCAAGCWGCAGCCACACAWTAGACCCAAGTACAATG              1607
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Fig. 1B

10063634.041302

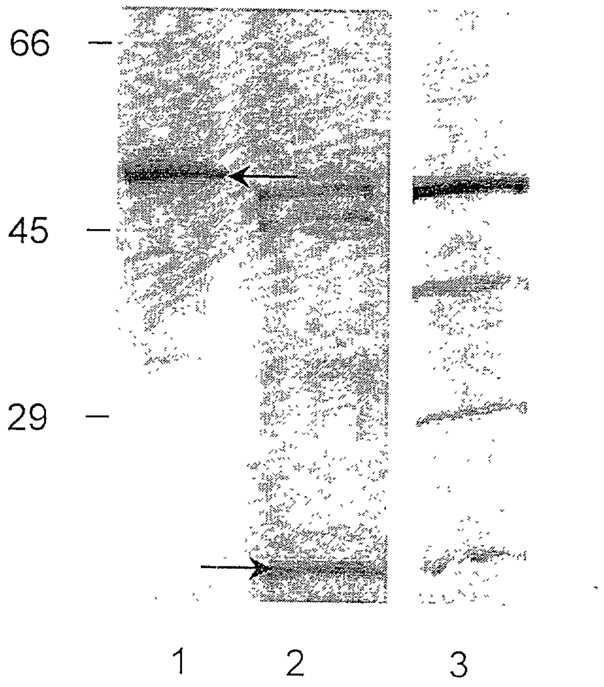


Fig. 2

```
                                         ↓
ECaP28     MNCKKILITTALISLMYSIPSISFSDTIQDGNMG-GN----FYISGKYVPSVSHFGSFSAKE-----ESKSTVGVFGLKH  70
ECa28SA2   .....VFTIS....SI.FL.NV.Y.NPVYGNS.-Y..----.......M...P...I...E.------.K.K.TV.Y...E  70
ECa28SA1   .KY..TFTV...VL.TSFTHF.P.YSPARASTIH--.----.......M.TA....I......------.QSF.KVLV..DQ  69
EChP28     ..Y..VF..S.....IS.L.GV....PA-GSGIN-..----.......M..A....V.....------.RNT........Q  69
OMP-1B     ..Y...FVSS......SIL.YQ..A.PVTSNDT.INDSREG....V..N..I...RK...E.APINGNTSI.KK.....K  80
OMP-1C     .....FF.....ALP.SFL.G.LL.EPV..DSVS-..----.......M..A....V.....------.KNP..ALY...Q  70
OMP-1D     ...E.FF.....TL..SFL.G..L..PV..D.IS-..----.......M..A....V.....------.RNT......IEQ  70
OMP-1E     .....FF.....V...SFL.G.....PV.GD.IS-..----..V....M..A....M.....------.KNP..ALY...Q  70
OMP-1F     .....FF...T.V...SFL.G.....AV.ND.V.-..----................V....Q------.RNT.T......Q  70
MAP-1      ......F..ST....VSFL.GV....V..EE.NPV.S----V...A..M.TA....KM.I..------D.RD.KA.....K  71
                                     VR1

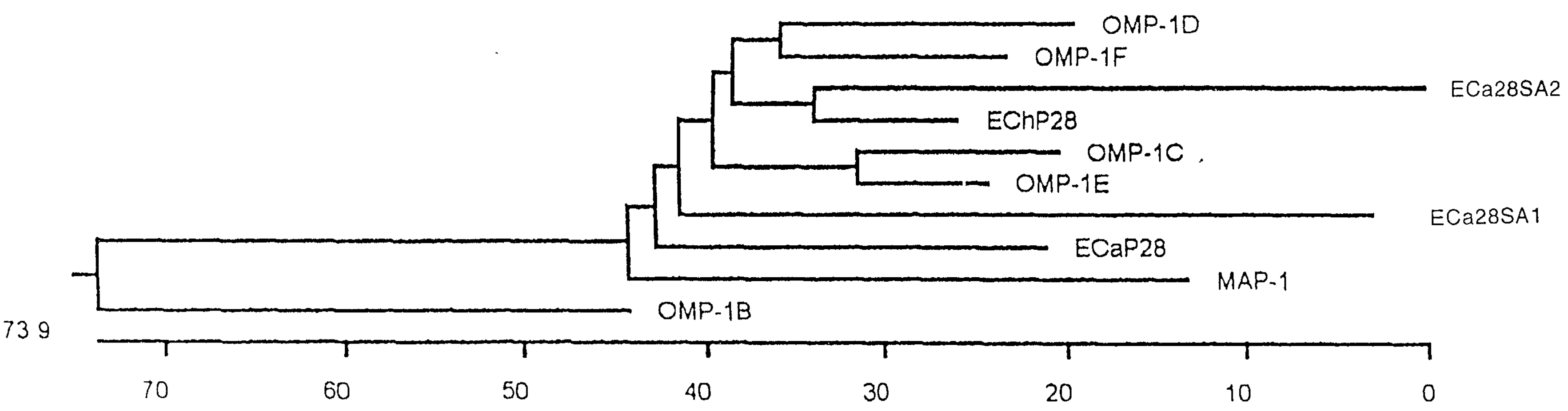
ECaP28     DWDGSPILKNKHAD-FTVPNYSFRYENNPFLGFAGAIGYSMGGPRIEFEISYEAFDVKSPNINYQNDAH--RYCALSH--  145
ECa28SA2   N.A.DA.SSQSPD.N..IR....K.AS.K.....V.....I.S....V.M.........NQGN.  (SEQ ID NO: 7)  133
ECa28SA1   RLSHNI.NN.DT.KSLK.Q....K.K...............I.NS...L.V.H.I..T.N.GN..L..S.--K......GS  147
EChP28     N....A.SNSSPN.V...S....K.................D.....L.V...T....NQGN..K.E..--.......--  145
OMP-1B     .------GDIAQSAN.NRTDPALEFQ..LIS..S.S...A.D.....L.AA.QK..A.N.DN.DT.SGDYYK.FG..RED  154
OMP-1C     ..N.-VSASSHADAD.NNKG...K.......................V...T....NQGG..K....--.....DR--  145
OMP-1D     ...RCV.SRTTLS.I........K....L.S...........D.....L.V.........NQGN..K.E..--..Y....--  146
OMP-1E     ..E.-ISSSSHNDNH.NNKG...K.....................V...V...T....NQGN..K....--.....GQ--  145
OMP-1F     .....T.S..SPENT.N......K............V..L.N.....L.M...T....NQGN..K....--K.Y..T.--  146
MAP-1      ....VKTPSGNTNSI..EKD...K............V....N........V...T...RN.GG..K....--M....----  145
               VR2
```

Fig. 3A

```
ECaP28      ----HTSAAME----ADKFVFLKNEGLIDISLAINACYDIINDKVPVSPYICAGIGTDLISMFEATSPKISYQGKLGISY  217
ECa28SA2                                                                                      133
ECa28SA1    HICSDGNSGDWYTAKT....L......L.V.FML......TTE.M.F.................T.QN.........LN.  227
EChP28      ------NS.ADMSSASNN.........L...FML.....VVGEGI.F............V......N..........L..  219
OMP-1B      AI------------ADK.Y.V.....ITFM..MV.T....TAEG..FI..A...V.A...NV.KDFNL.F.....I....  222
OMP-1C      ----KA.ST---NAT.SHY.L......L....ML.....VVSEGI.F.......V..........IN..........L..  218
OMP-1D      ----LLGTETQIDGAGSAS...I....L.K.FML.....V.SEGI.F.........I..V.....IN..........L..  222
OMP-1E      ----QDNSG---IPKTS.Y.L..S...L...FML........ESI.L.......V...........N..........L..  218
OMP-1F      ------NSGGKLSNAG...........L....ML.....V.SEGI.F.......V..........IN..........L..  220
MAP-1       ------DT.SSSTAG.TTS.MV...N.T....ML......ML.GM.....V........V.VIN..N..L..........  219
                     VR3

ECaP28      SINPETSVFIGGHFHRIIGNEFRDIPA---IVPSNSTTISGPQF-ATVTLNVCHFGLELGGRFNF  (SEQ ID NO:2)   278
ECa28SA2                                                                                      133
ECa28SA1    T..SRV...A.....KV.....KG..T---LL.DG.NIKVQQS--.....D.......I.S..F.  (SEQ ID NO:8)   287
EChP28      ..S..A.........KV.........T---.I.TG..LAGKGNYP.I.I.D.....I......A.  (SEQ ID NO:9)   281
OMP-1B      P.T..V.A....YY.GV...N.NK..VITPV.LEGAPQTTS----.L..IDTGY..G.V.V..T.  (SEQ ID NO:10)  283
OMP-1C      .....A...V.....KVA.......ST---LKAFATPSSAATPDL.....S.....V........  (SEQ ID NO:11)  280
OMP-1D      P.S..A.........KV.........T---MI..E.ALAGKGNYP.I...D.FY..I........QL(SEQ ID NO:12)  286
OMP-1E      .....A.........KV.........T---LKAFVTSS--ATPDL.I...S.....I........  (SEQ ID NO:13)  278
OMP-1F      ..S..A...V.....KV..........---MI..T..LTGN-H.-TI...S.....V........  (SEQ ID NO:14)  280
MAP-1       .....A.I........V.....K..ATSKVFTS.GNASSAVSPGF.SAI.D.....I.I....V.  (SEQ ID NO:15)  284
                                                 VR4
```

Fig. 3B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OMP-1F
ECa28SA2
EChP28
OMP-1C
OMP-1E
ECa28SA1
ECaP28
MAP-1
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73 9
70
60
50
40
30
20
10
0

Fig. 4

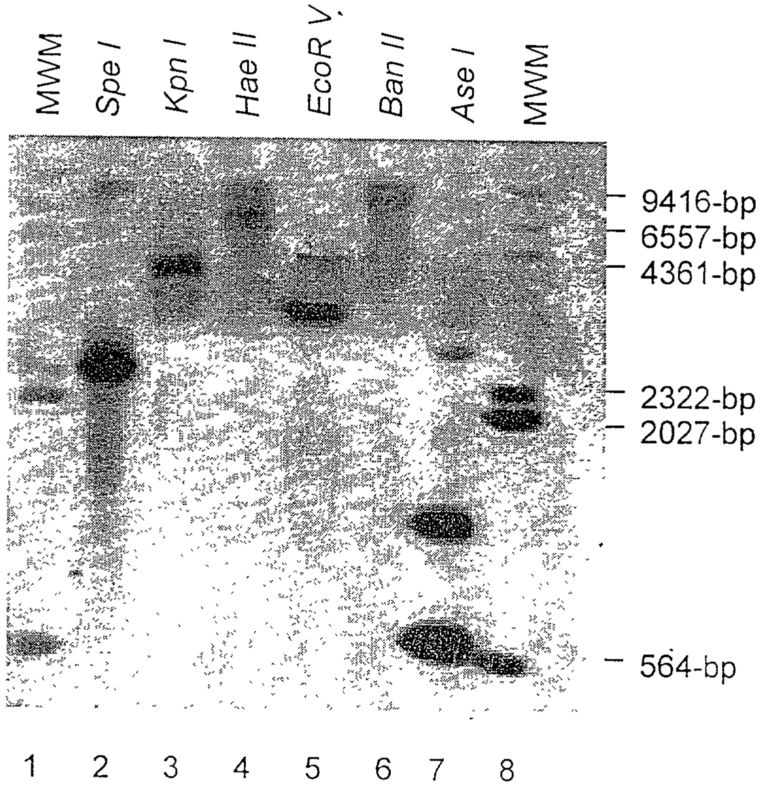
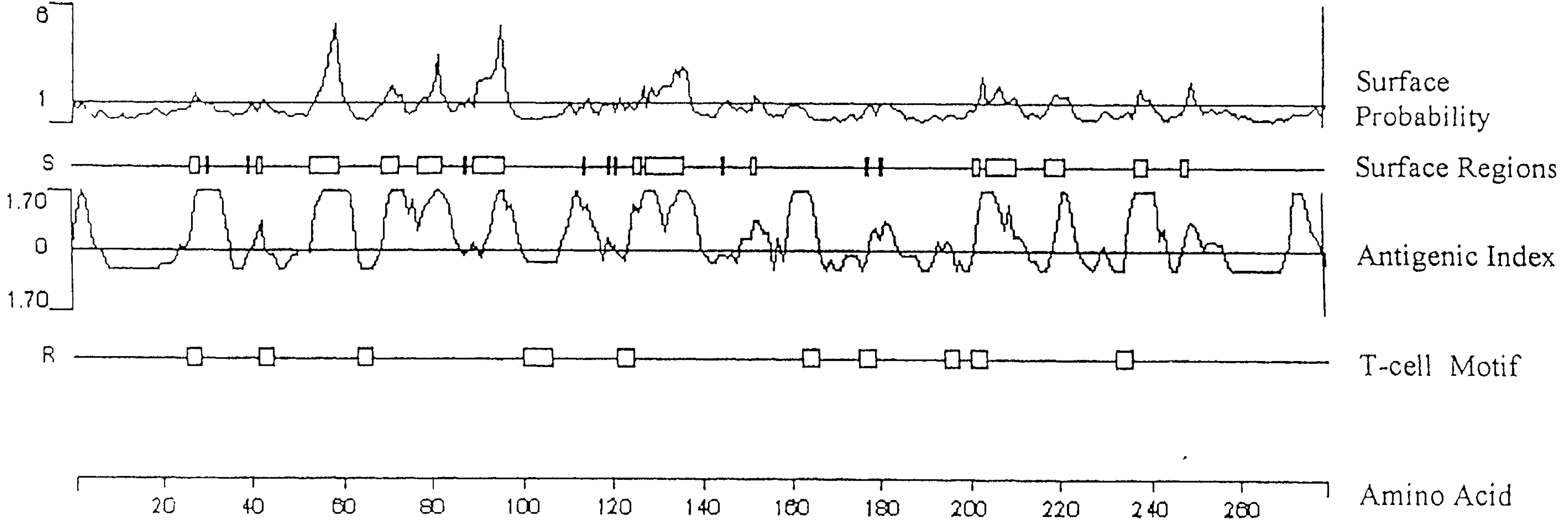


Fig. 5

10063694.041302

E. canis P28 (Jake)



E. chaffeensis P28 (Arkansas)

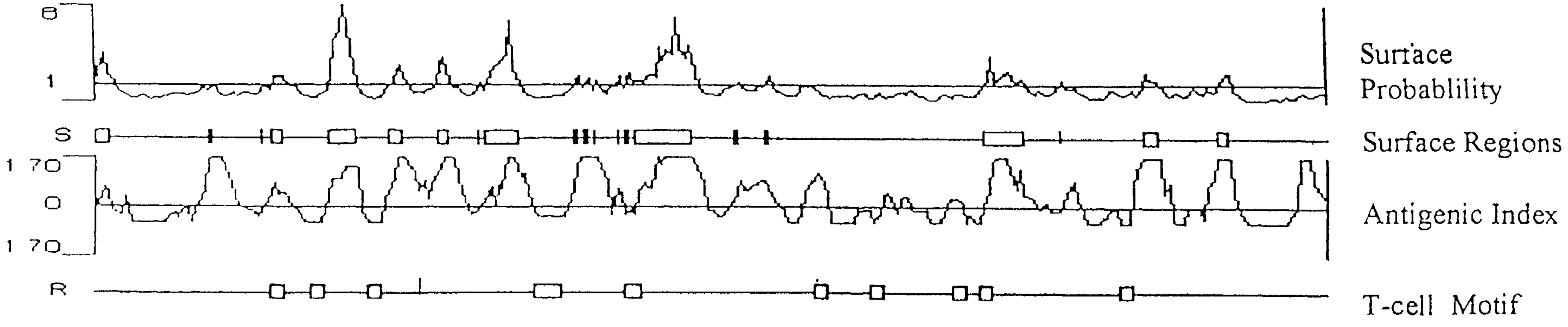


Fig. 6

Eca28SA2

ATGAATTGTAAAAAAGTTTTCACAATAAGTGCATTGATATCATCCATATACTTCCTACCT 60
M N C K K V F T I S A L I S S I Y F L P

AATGTCTCATACTCTAACCCAGTATATGGTAACAGTATGTATGGTAATTTTTACATATCA 120
N V S Y S N P V Y G N S M Y G N F Y I S

GGAAAGTACATGCCAAGTGTTCCTCATTTTGGAATTTTTTCAGCTGAAGAAGAGAAAAAA 180
G K Y M P S V P H F G I F S A E E E K K

AAGACAACTGTAGTATATGGCTTAAAAGAAAACTGGGCAGGAGATGCAATATCTAGTCAA 240
K T T V V Y G L K E N W A G D A I S S Q

AGTCCAGATGATAATTTTACCATTCGAAATTACTCATTCAAGTATGCAAGCAACAAGTTT 300
S P D D N F T I R N Y S F K Y A S N K F

TTAGGGTTTGCAGTAGCTATTGGTTACTCGATAGGCAGTCCAAGAATAGAAGTTGAGATG 360
L G F A V A I G Y S I G S P R I E V E M

TCTTATGAAGCATTTGATGTGAAAAATCCAGGTGATAATTACAAAAACGGTGCTTACAGG 420
S Y E A F D V K N P G D N Y K N G A Y R

TATTGTGCTTTATCTCATCAAGATGATGCGGATGATGACATGACTAGTGCAACTGACAAA 480
Y C A L S H Q D D A D D D M T S A T D K

TTTGTATATTTAATTAATGAAGGATTACTTAACATATCATTTATGACAAACATATGTTAT 540
F V Y L I N E G L L N I S F M T N I C Y

GAAACAGCAAGCAAAAATATACCTCTCTCTCCTTACATATGTGCAGGTATTGGTACTGAT 600
E T A S K N I P L S P Y I C A G I G T D

TTAATTCACATGTTTGAAACTACACATCCTAAAATTTCTTATCAAGGAAAGCTAGGGTTG 660
L I H M F E T T H P K I S Y Q G K L G L

Fig. 7A

```
GCCTACTTCGTAAGTGCAGAGTCTTCGGTTTCTTTTGGTATATATTTTCATAAAATTATA  720
 A  Y  F  V  S  A  E  S  S  V  S  F  G  I  Y  F  H  K  I  I

AATAATAAGTTTAAAAATGTTCCAGCCATGGTACCTATTAACTCAGACGAGATAGTAGGA  780
 N  N  K  F  K  N  V  P  A  M  V  P  I  N  S  D  E  I  V  G

CCACAGTTTGCAACAGTAACATTAAATGTATGCTACTTTGGATTAGAACTTGGATGTAGG  840
 P  Q  F  A  T  V  T  L  N  V  C  Y  F  G  L  E  L  G  C  R
          (SEQ ID NO: 3)
TTCAACTTCTAATTTCGTGGTACACATATCACGAAGCTAAAATTGTTTTTTATCTCTGC  900
 F  N  F  * (SEQ ID NO: 4)

TGTATACAAGAGAAAAAATAGTAGTGAAAATTACCTAACAATATGACAGTACAAGTTTAC  960
CAAGCTTATTCTCACAAAACTTCTTGTGTCTTTTATCTCTTTACAATGAAATGTACACTT  1020
AGCTTCACTACTGTAGAGTGTGTTTATCAATGCTTTGTTTATTAATACTCTACATAATAT  1080
GTTAAATTTTTCTTACAAAACTCACTAGTAATTTATACTAGAATATATATTCTGACTTGT  1140
                                               (SEQ ID NO: 31)
 ECa28SA3
ATTTGCTTTATACTTCCACTATTGTTAATTTATTTTCACTATTTTAGGTGTAATATGAAT  1200
                                                       M  N

TGCAAAAAAATTCTTATAACAACTGCATTAATGTCATTAATGTACTATGCTCCAAGCATA  1260
 C  K  K  I  L  I  T  T  A  L  M  S  L  M  Y  Y  A  P  S  I

TCTTTTTCTGATACTATACAAGACGATAACACTGGTAGCTTCTACATCAGTGGAAAATAT  1320
 S  F  S  D  T  I  Q  D  D  N  T  G  S  F  Y  I  S  G  K  Y

GTACCAAGTGTTTCACATTTTGGTGTTTTCTCAGCTAAAGAAGAAAGAAACTCAACTGTT  1380
 V  P  S  V  S  H  F  G  V  F  S  A  K  E  E  R  N  S  T  V

GGAGTTTTTGGATTAAAACATGATTGGAATGGAGGTACAATATCTAACTCTTCTCCAGAA  1440
 G  V  F  G  L  K  H  D  W  N  G  G  T  I  S  N  S  S  P  E
```

Fig. 7B

10062624.013102

AATATATTCACAGTTCAAAATTATTCGTTTAAATACGAAAACAACCCATTCTTAGGGTTT 1500
N I F T V Q N Y S F K Y E N N P F L G F

GCAGGAGCTATTGGTTATTCAATGGGTGGCCCAAGAATAGAACTTGAAGTTCTGTACGAG 1560
A G A I G Y S M G G P R I E L E V L Y E

ACATTCGATGTGAAAAATCAGAACAATAATTATAAGAACGGCGCACACAGATACTGTGCT 1620
T F D V K N Q N N N Y K N G A H R Y C A

TTATCTCATCATAGTTCAGCAACAAGCATGTCCTCCGCAAGTAACAAATTTGTTTTCTTA 1680
L S H H S S A T S M S S A S N K F V F L

AAAAATGAAGGGTTAATTGACTTATCATTTATGATAAATGCATGCTATGACATAATAATT 1740
K N E G L I D L S F M I N A C Y D I I I

GAAGGAATGCCTTTTTCACCTTATATTTGTGCAGGTGTTGGTACTGATGTTGTTTCCATG 1800
E G M P F S P Y I C A G V G T D V V S M

TTTGAAGCTATAAATCCTAAAATTTCTTACCAAGGAAAACTAGGATTAGGTTATAGTATA 1860
F E A I N P K I S Y Q G K L G L G Y S I

AGTTCAGAAGCCTCTGTTTTTATCGGTGGACACTTTCACAGAGTCATAGGTAATGAATTT 1920
S S E A S V F I G G H F H R V I G N E F

AGAGACATCCCTGCTATGGTTCCTAGTGGATCAAATCTTCCAGAAAACCAATTTGCAATA 1980
R D I P A M V P S G S N L P E N Q F A I
(SEQ ID NO: 5)
GTAACACTAAATGTGTGTCACTTTGGCATAGAACTTGGAGGAAGATTTAACTTC**TGA** 2031
V T L N V C H F G I E L G G R F N F *
(SEQ ID NO: 6)

Fig. 7C

10065624.013102

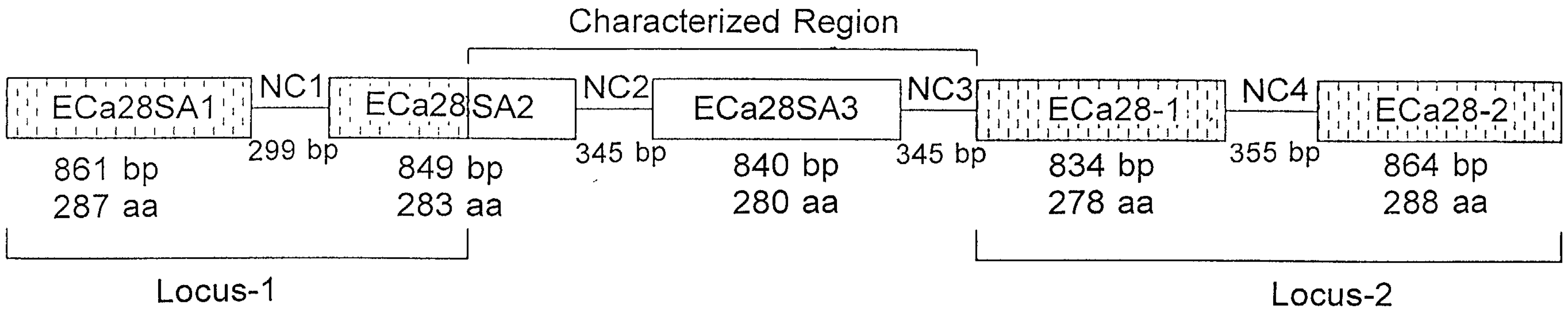
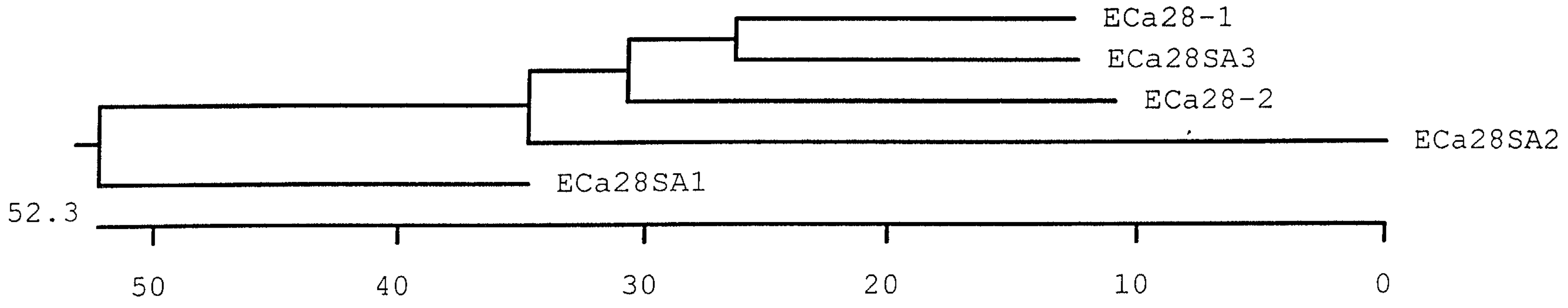


Fig. 8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ECa28SA3
ECa28-2
ECa28SA2
ECa28SA1
52.3
50
40
30
20
10
0

Fig. 9

```
1     TAATACTTCTATTGT-ACATGTTAAAAATAGTACTAGTTTGCTTCTGTGGTT--TATAAACGCAAGAGAGAA--   28nc1
1     ....TTCGTGG.A--C....A.C.CG..-GC..AA.T.G.TT..T.A.CTC.GC.G..T..AAG...A.A..TA   28nc2
1     .G..TT.AT.G...CC....A........GA.CTA.AC...T..T.A.TA..GC..C.T..AA..A.A....AA   28nc3
1     ....TT.AT.G...CC....A........GA.CTA.AC...T..T.AWTA..GC..C.T..AA..A.A-...AA   28nc4

70    ATAGT------------TAGTAATAAATTAGAAAG------TTAAA--TATT---AGAAAAGT-CA           28nc1
72    G....G--AAAATTACC..AC....TGAC..T.CAAGTTTACC..GCT....CTC.C....C.T.T           28nc2
75    .....GGCAAAAGAATG...C.....GAGG.GGG.GGGGGAC....TT..CCTTC--T.TTC.T.T           28nc3
74    .....GGCAAAAGAATG...C.....GAGG.GGG.GGGGGACC...TT...CTTC--T.TGC.T.C           28nc4

112   TATGTTTTTCATTGTCATTGAT-ACTCAACTA----AAAGTAGTAT----------AAATGT------------   28nc1
136   .G...C...T..CTCT--.T.CA.-.G..A.-GTAC.-CT...CT.CACTACTGTAG.G...GTTTATCAATGC   28nc2
139   A..A..C..T---ACT.------.T....A..GCAC..CTC.A.GCTTCCA-GG-A....A.GT-TTCTAATAT   28nc3
138   C.A......TCYC.CT...T..G...T..AC.ACAG..G...A...CCTCACGG-A...CT.ATCTTCAAATAT   28nc4

159   --TACTTATTAATAAT-TTTACGTAGTATATTAAATTTCCCTTACAAAAGCCACTAGTATTTTATA           28nc1
205   TT.GT.........--C.C...A..A...G........TT.........CT........A......           28nc2
202   TT..T......CC...CC...TA..A.............T.........AT.T...A.G.......           28nc3
211   TT..T......CC...C-...TA..A.............T.........AT...............           28nc4

222   CTAAAAGC-TATACTTTGGCTTGTATTTAATTTGTATTTTTACTACTGTTAATTTACTT-TCACTGTT---TCT   28nc1
269   .-T.G.ATA....T.C..A.........GC...A..C..CC....T..........T..-.....A..---.TA   28nc2
268   ..T..TATA....T.C.............C....C.C..CC....T..........T..-.....A..---.TA   28nc3
276   .C-...ATA....T.C..A....CT...CT.C..C.C..C.....T.T........T..G.....A..AGG.TA   28nc4
                                         -35                 -10

292   GGTGTAAAT 28nc1     (SEQ ID NO: 30)
338   .......-. 28nc2     (SEQ ID NO: 31)
339   .......-. 28nc3     (SEQ ID NO: 32)
339   TA-A...-W 28nc4     (SEQ ID NO: 33)
          RBS
```

Fig. 10

10062624.013102

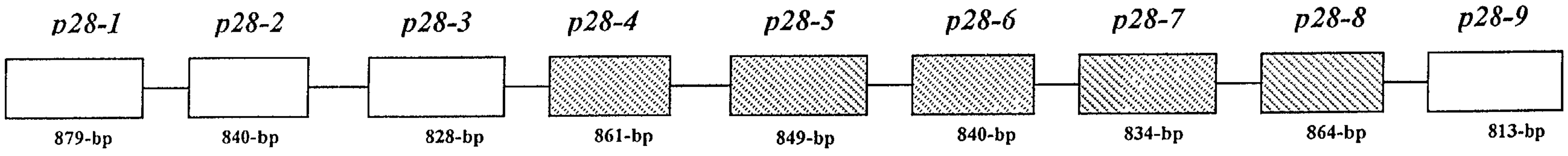

Fig. 11

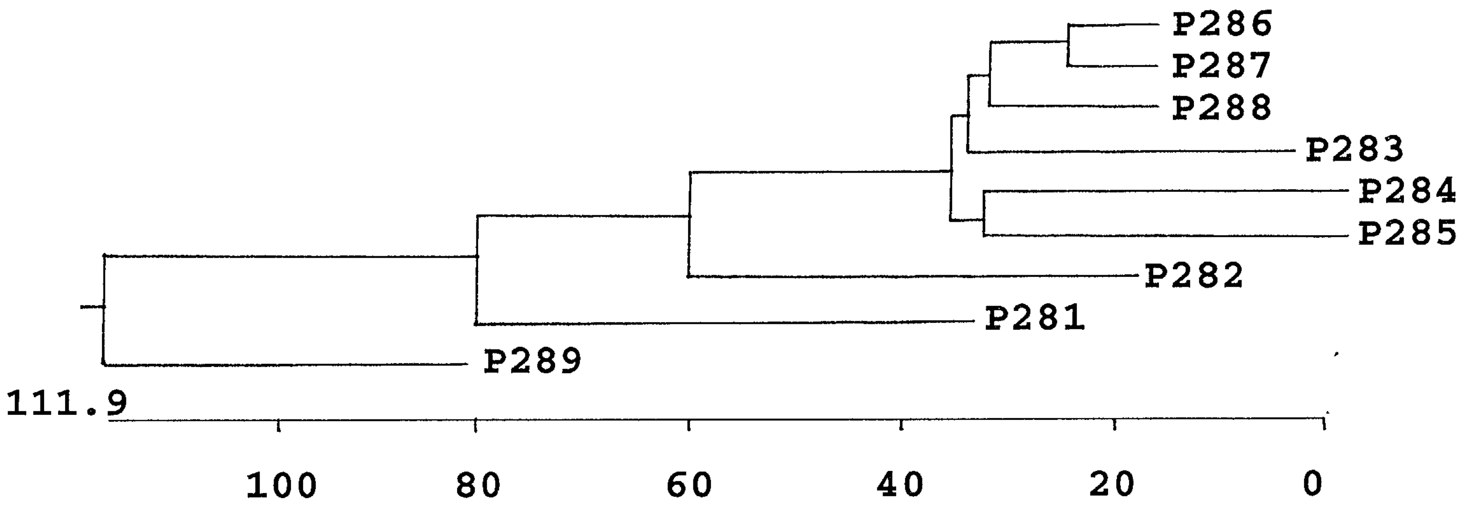
P286
P287
P288
P283
P284
P285
P282
P281
P289
111.9
100
80
60
40
20
0

Fig. 12

```
ATGAATAATAAACTCAAATTTACTATAATAAACACAGTATTAGTATGCTTATTGTCATTA 60
M  N  N  K  L  K  F  T  I  I  N  T  V  L  V  C  L  L  S  L

CCTAATATATCTTCCTCAAAGGCCATAAACAATAACGCTAAAAAGTACTACGGATTATAT 120
P  N  I  S  S  S  K  A  I  N  N  N  A  K  K  Y  Y  G  L  Y

ATCAGTGGACAATATAAACCCAGTGTTTCTGTTTTCAGTAATTTTTCAGTTAAAGAAACC 180
I  S  G  Q  Y  K  P  S  V  S  V  F  S  N  F  S  V  K  E  T

AATGTCATAACTAAAAACCTTATAGCTTTAAAAAAAGATGTTGACTCTATTGAAACCAAG 240
N  V  I  T  K  N  L  I  A  L  K  K  D  V  D  S  I  E  T  K

ACTGATGCCAGTGTAGGTATTAGTAACCCATCAAATTTTACTATCCCCTATACAGCTGTA 300
T  D  A  S  V  G  I  S  N  P  S  N  F  T  I  P  Y  T  A  V

TTTCAAGATAATTCTGTCAATTTCAATGGAACTATTGGTTACACCTTTGCTGAAGGTACA 360
F  Q  D  N  S  V  N  F  N  G  T  I  G  Y  T  F  A  E  G  T

AGAGTTGAAATAGAAGGTTCTTATGAGGAATTTGATGTTAAAAACCCTGGAGGCTATACA 420
R  V  E  I  E  G  S  Y  E  E  F  D  V  K  N  P  G  G  Y  T

CTAAGTGATGCCTATCGCTATTTTGCATTAGCACGTGAAATGAAAGGTAATAGTTTTACA 480
L  S  D  A  Y  R  Y  F  A  L  A  R  E  M  K  G  N  S  F  T

CCTAAAGAAAAAGTTTCTAATAGTATTTTTCACACTGTAATGAGAAATGATGGATTATCT 540
P  K  E  K  V  S  N  S  I  F  H  T  V  M  R  N  D  G  L  S

ATAATATCTGTTATAGTAAATGTTTGCTACGATTTCTCTTTGAACAATTTGTCAATATCG 600
I  I  S  V  I  V  N  V  C  Y  D  F  S  L  N  N  L  S  I  S

CCTTACATATGTGGAGGAGCAGGGGTAGATGCTATAGAATTCTTCGATGTATTACACATT 660
P  Y  I  C  G  G  A  G  V  D  A  I  E  F  F  D  V  L  H  I

AAGTTTGCATATCAAAGCAAGCTAGGTATTGCTTATTCTCTACCATCTAACATTAGTCTC 720
K  F  A  Y  Q  S  K  L  G  I  A  Y  S  L  P  S  N  I  S  L

TTTGCTAGTTTATATTACCATAAAGTAATGGGCAATCAATTTAAAAATTTAAATGTCCAA 780
F  A  S  L  Y  Y  H  K  V  M  G  N  Q  F  K  N  L  N  V  Q

CATGTTGCTGAACTTGCAAGTATACCTAAAATTACATCCGCAGTTGCTACACTTAATATT 840
H  V  A  E  L  A  S  I  P  K  I  T  S  A  V  A  T   L  N  I

GGTTATTTTGGAGGTGAAATTGGTGCAAGATTGACATTT  (SEQ ID No. 39)     879
G  Y  F  G  G  E  I  G  A  R  L  T  F    (SEQ ID NO. 40)
```

Fig. 13

ATGAATTATAAGAAAATTCTAGTAAGAAGCGCGTTAATCTCATTAATGTCAATCTTACCA 60
M N Y K K I L V R S A L I S L M S I L P
TATCAGTCTTTTGCAGATCCTGTAGGTTCAAGAACTAATGATAACAAAGAAGGCTTCTAC 120
Y Q S F A D P V G S R T N D N K E G F Y
ATTAGTGCAAAGTACAATCCAAGTATATCACACTTTAGAAAATTCTCTGCTGAAGAAACT 180
I S A K Y N P S I S H F R K F S A E E T
CCTATTAATGGAACAAATTCTCTCACTAAAAAAGTTTTCGGACTAAAGAAAGATGGTGAT 240
P I N G T N S L T K K V F G L K K D G D
ATAACAAAAAAAGACGATTTTACAAGAGTAGCTCCAGGCATTGATTTTCAAAATAACTTA 300
I T K K D D F T R V A P G I D F Q N N L
ATATCAGGATTTTCAGGAAGTATTGGTTACTCTATGGACGGACCAAGAATAGAACTTGAA 360
I S G F S G S I G Y S M D G P R I E L E
GCTGCATATCAACAATTTAATCCAAAAAACACCGATAACAATGATACTGATAATGGTGAA 420
A A Y Q Q F N P K N T D N N D T D N G E
TACTATAAACATTTTGCATTATCTCGTAAAGATGCAATGGAAGATCAGCAATATGTAGTA 480
Y Y K H F A L S R K D A M E D Q Q Y V V
CTTAAAAATGACGGCATAACTTTTATGTCATTGATGGTTAATACTTGCTATGACATTACA 540
L K N D G I T F M S L M V N T C Y D I T
GCTGAAGGAGTATCTTTCGTACCATATGCATGTGCAGGTATAGGAGCAGATCTTATCACT 600
A E G V S F V P Y A C A G I G A D L I T
ATTTTTAAAGACCTCAATCTAAAATTTGCTTACCAAGGAAAAATAGGTATTAGTTACCCT 660
I F K D L N L K F A Y Q G K I G I S Y P
ATCACACCAGAAGTCTCTGCATTTATTGGTGGATACTACCATGGCGTTATTGGTAATAAA 720
I T P E V S A F I G G Y Y H G V I G N K
TTTGAGAAGATACCTGTAATAACTCCTGTAGTATTAAATGATGCTCCTCAAACCACATCT 780
F E K I P V I T P V V L N D A P Q T T S
GCTTCAGTAACTCTTGACGTTGGATACTTTGGCGGAGAAATTGGAATGAGGTTCACCTTC 840
(SEQ ID No. 41)
A S V T L D V G Y F G G E I G M R F T F
(SEQ ID No. 42)

Fig. 14

ATGAACTGTAAAAAAATTCTTATAACAACTACATTGGTATCACTAACAATTCTTTTACCT 60

M N C K K I L I T T T L V S L T I L L P

GGCATATCTTTCTCCAAACCAATACATGAAAACAATACTACAGGAAACTTTTACATTATT 120

G I S F S K P I H E N N T T G N F Y I I

GGAAAATATGTACCAAGTATTTCACATTTTGGGAACTTTTCAGCTAAAGAAGAAAAAAAC 180

G K Y V P S I S H F G N F S A K E E K N

ACAACAACTGGAATTTTTGGATTAAAAGAATCATGGACTGGTGGTATCATCCTTGATAAA 240

T T T G I F G L K E S W T G G I I L D K

GAACATGCAGCTTTTAATATCCCAAATTATTCATTTAAATATGAAAATAATCCATTTTTA 300

E H A A F N I P N Y S F K Y E N N P F L

GGATTTGCAGGGGTAATTGGCTATTCAATAGGTAGTCCAAGAATAGAATTTGAAGTATCA 360

G F A G V I G Y S I G S P R I E F E V S

TACGAGACATTCGATGTACAAAATCCAGGAGATAAGTTTAACAATGATGCACATAAGTAT 420

Y E T F D V Q N P G D K F N N D A H K Y

TGTGCTTTATCCAATGATTCCAGTAAAACAATGAAAAGTGGTAAATTCGTTTTTCTCAAA 480

C A L S N D S S K T M K S G K F V F L K

AATGAAGGATTAAGTGACATATCACTCATGTTAAATGTATGTTATGATATAATAAACAAA 540

N E G L S D I S L M L N V C Y D I I N K

AGAATGCCTTTTTCACCTTACATATGTGCAGGCATTGGTACTGACTTAATATTCATGTTT 600

R M P F S P Y I C A G I G T D L I F M F

GACGCTATAAACCATAAAGCTGCTTATCAAGGAAAATTAGGTTTTAATTATCCAATAAGC 660

D A I N H K A A Y Q G K L G F N Y P I S

CCAGAAGCTAACATTTCTATGGGTGTGCACTTTCACAAAGTAACAAACAACGAGTTTAGA 720

P E A N I S M G V H F H K V T N N E F R

GTTCCTGTTCTATTAACTGCTGGAGGACTCGCTCCAGATAATCTATTTGCAATAGTAAAG 780

V P V L L T A G G L A P D N L F A I V K

TTGAGTATATGTCATTTTGGGTTAGAATTTGGGTACAGGGTCAGTTTT (SEQ ID No. 43) 828

L S I C H F G L E F G Y R V S F (SEQ ID NO. 44)

Fig. 15

ATGAATTACAAAAGATTTGTTGTAGGTGTTACGCTGAGTACATTTGTTTTTTTCTTATCT 60
M N Y K R F V V G V T L S T F V F F L S

GATGGTGCTTTTTCTGATGCAAATTTTTCTGAAGGGAGGAGAGGACTTTATATAGGTAGT 120
D G A F S D A N F S E G R R G L Y I G S

CAGTATAAAGTTGGTATTCCCAATTTTAGTAATTTTTCAGCTGAAGAAACAATTCCTGGT 180
Q Y K V G I P N F S N F S A E E T I P G

ATTACAAAAAAGATTTTTGCGTTAGGTCTTGATAAGTCTGAGATAAATACTCACAGCAAT 240
I T K K I F A L G L D K S E I N T H S N

TTTACACGATCATATGACCCTACTTATGCAAGCAGTTTTGCAGGGTTTAGTGGTATCATT 300
F T R S Y D P T Y A S S F A G F S G I I

GGATATTATGTTAATGACTTTAGGGTAGAATTTGAAGGTTCTTATGAGAATTTTGAACCT 360
G Y Y V N D F R V E F E G S Y E N F E P

GAAAGACAATGGTACCCTGAGAATAGCCAAAGCTACAAATTTTTTGCTTTGTCTCGAAAT 420
E R Q W Y P E N S Q S Y K F F A L S R N

GCTACAAATAGTGATAATAAGTTTATAGTACTAGAGAATAACGGCGTTGTTGACAAGTCT 480
A T N S D N K F I V L E N N G V V D K S

CTTAATGTAAATGTTTGTTATGATATTGCTAGTGGTAGTATTCCTTTAGCACCTTATATG 540
L N V N V C Y D I A S G S I P L A P Y M

TGTGCTGGTGTTGGTGCAGATTATATAAAGTTTTTAGGTATATCATTGCCTAAGTTTTCT 600
C A G V G A D Y I K F L G I S L P K F S

TATCAAGTTAAGTTTGGTGTCAACTACCCTCTAAATGTTAATACTATGTTGTTTGGTGGG 660
Y Q V K F G V N Y P L N V N T M L F G G

GGTTATTACCATAAGGTTGTAGGTGATAGGCATGAGAGAGTAGAAATAGCTTACCATCCT 720
G Y Y H K V V G D R H E R V E I A Y H P

ACTGCATTATCTGACGTTCCTAGAACTACTTCAGCTTCTGCTACTTTAAATACTGATTAT 780
T A L S D V P R T T S A S A T L N T D Y

TTTGGTTGGGAGATTGGATTTAGATTTGCGCTA (SEQ ID No. 45) 813
F G W E I G F R F A L (SEQ ID No. 46)

Fig. 16